```
=============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2008; month=5; day=30; hr=12; min=17; sec=48; ms=565; ]
=============================================================



*************************************************************
Reviewer Comments:
<210>   30
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer


<400>   30
gcttatggcg cgcctcagga ctggagcttg ctccgc
36n
21


Please delete the extra n which appears beside the total number of bases
36 and also remove the end of file text which is below the bases(21)  as
shown in the attachment above.
*************************************************************
```

Application No: 10590956   Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-09 16:08:23.466
Finished: 2008-05-09 16:08:25.990
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 524 ms
Total Warnings: 24
Total Errors: 7
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

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          Input Set:


          Output Set:



            Started:   2008-05-09 16:08:23.466
           Finished:   2008-05-09 16:08:25.990
            Elapsed:   0 hr(s) 0 min(s) 2 sec(s) 524 ms
     Total Warnings:   24
       Total Errors:   7
 No. of SeqIDs Defined:   30
  Actual SeqID Count:   30
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
E 342	'n' position not defined found at POS: 39 SEQID(30)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 39 SEQID(30)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (1)
E 323	Invalid/missing amino acid numbering SEQID (30) POS (1)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (5)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (10)
E 253	The number of bases differs from <211> Input: 36 Calculated:39

atgtatcgga agttggccgt catctcggcc ttcttggcca cagctcgtgc tcagtcggcc   60
tgcactctcc aatcggagac tcacccgcct ctgacatggc agaaatgctc gtctggtggc   120
acttgcactc aacagacagg ctccgtggtc atcgacgcca actggcgctg gactcacgct   180
acgaacagca gcacgaactg ctacgatggc aacacttgga gctcgaccct atgtcctgac   240
aacgagacct gcgcgaagaa ctgctgtctg gacggtgccg cctacgcgtc cacgtacgga   300
gttaccacga gcggtaacag cctctccatt ggctttgtca cccagtctgc gcagaagaac   360
gttggcgctc gcctttacct tatggcgagc gacacgacct accaggaatt caccctgctt   420
ggcaacgagt tctctttcga tgttgatgtt tcgcagctgc cgtaagtgac ttaccatgaa   480
cccctgacgt atcttcttgt gggctcccag ctgactggcc aatttaaggt gcggcttgaa   540
cggagctctc tacttcgtgt ccatggacgc ggatggtggc gtgagcaagt atcccaccaa   600
caccgctggc gccaagtacg gcacgggta ctgtgacagc cagtgtcccc gcgatctgaa   660
gttcatcaat ggccaggcca acgttgaggg ctgggagccg tcatccaaca acgcaaacac   720
gggcattgga ggacacggaa gctgctgctc tgagatggat atctgggagg ccaactccat   780
ctccgaggct cttacccccc acccttgcac gactgtcggc caggagatct gcgagggtga   840
tgggtgcggc ggaacttact ccgataacag atatggcggc acttgcgatc ccgatggctg   900
cgactggaac ccataccgcc tgggcaacac cagcttctac ggccctggct caagctttac   960
cctcgatacc accaagaaat tgaccgttgt cacccagttc gagacgtcgg tgccatcaa   1020
ccgatactat gtccagaatg gcgtcacttt ccagcagccc aacgccgagc ttggtagtta   1080
ctctggcaac gagctcaacg atgattactg cacagctgag gaggcagaat cggcggatc   1140
ctctttctca gacaagggcg gcctgactca gttcaagaag ctacctctg gcggcatggt   1200
tctggtcatg agtctgtggg atgatgtgag tttgatggac aaacatgcgc gttgacaaag   1260
agtcaagcag ctgactgaga tgttacagta ctacgccaac atgctgtggc tggactccac   1320
ctacccgaca aacgagacct cctccacacc cggtgccgtg cgcggaagct gctccaccag   1380
ctccggtgtc cctgctcagg tcgaatctca gtctcccaac gccaggtca ccttctccaa   1440
catcaagttc ggacccattg gcagcaccgg caaccctagc ggcggcaacc tccccggcgg   1500
aaacccgcct ggcaccacca ccacccgccg cccagccact accactggaa gctctcccgg   1560

acctactagt   1570

<210> 2

<211> 51
<212> DNA
<213> Trichoderma reesei

<400> 2
atgtatcgga agttggccgt catctcggcc ttcttggcca cagctcgtgc t   51

<210> 3
<211> 1438
<212> DNA
<213> Trichoderma reesei

<400> 3
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actcacgcta cgaacagcag cacgaactgc tacgatggca cacttggag ctcgacccta   180
tgtcctgaca acgagacctg cgcgaagaac tgctgtctgg acggtgccgc ctacgcgtcc   240
acgtacggag ttaccacgag cggtaacagc ctctccattg ctttgtcac ccagtctgcg   300
cagaagaacg ttggcgctcg cctttacctt atggcgagcg acacgaccta ccaggaattc   360
accctgcttg caacgagtt ctctttcgat gttgatgttt cgcagctgcc gtaagtgact   420
taccatgaac ccctgacgta tcttcttgtg ggctcccagc tgactggcca atttaaggtg   480
cggcttgaac ggagctctct acttcgtgtc catggacgcg gatggtggcg tgagcaagta   540
tcccaccaac accgctggcg ccaagtacgg cacggggtac tgtgacagcc agtgtccccg   600
cgatctgaag ttcatcaatg ccaggccaa cgttgagggc tgggagccgt catccaacaa   660
cgcaaacacg ggcattggag acacggaag ctgctgctct gagatggata tctgggaggc   720
caactccatc tccgaggctc ttacccccca cccttgcacg actgtcggcc aggagatctg   780
cgagggtgat gggtgcggcg gaacttactc cgataacaga tatggcggca cttgcgatcc   840
cgatggctgc gactggaacc cataccgcct gggcaacacc agcttctacg ccctggctc   900
aagctttacc ctcgatacca ccaagaaatt gaccgttgtc acccagttcg agacgtcggg   960
tgccatcaac cgatactatg tccagaatgg cgtcactttc cagcagccca cgccgagct   1020
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cggcggatcc tctttctcag acaagggcgg cctgactcag ttcaagaagg ctacctctgg   1140
cggcatggtt ctggtcatga gtctgtggga tgatgtgagt ttgatggaca acatgcgcg   1200
ttgacaaaga gtcaagcagc tgactgagat gttacagtac tacgccaaca tgctgtggct   1260
ggactccacc tacccgacaa acgagacctc ctccacaccc ggtgccgtgc gcggaagctg   1320
ctccaccagc tccggtgtcc ctgctcaggt cgaatctcag tctcccaacg ccaaggtcac   1380
cttctccaac atcaagttcg gacccattgg cagcaccggc aaccctagcg gcggcaac   1438

<210> 4
<211> 81
<212> DNA
<213> Trichoderma reesei

<400> 4
cctcccggcg gaaacccgcc tggcaccacc accacccgcc gcccagccac taccactgga   60
agctctcccg gacctactag t   81

<210> 5
<211> 480
<212> PRT
<213> Trichoderma reesei

<400> 5

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Met Tyr Arg Lys Leu Ala Val Ile Ser Ala Phe Leu Ala Thr Ala Arg
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Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
            20                  25                  30
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
        35                  40                  45
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
    50                  55                  60
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
65                  70                  75                  80
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
                85                  90                  95
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
            100                 105                 110
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
    115                 120                 125
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
    130                 135                 140
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
145                 150                 155                 160
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
            165                 170                 175
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
            180                 185                 190
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
        195                 200                 205
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
    210                 215                 220
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
225                 230                 235                 240
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
            245                 250                 255
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
            260                 265                 270
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
        275                 280                 285
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
    290                 295                 300
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
305                 310                 315                 320
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
            325                 330                 335
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
            340                 345                 350
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
        355                 360                 365
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
    370                 375                 380
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
385                 390                 395                 400
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
            405                 410                 415
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
            420                 425                 430
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
    435                 440                 445
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
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Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Ser
465   470   475   480

<210> 6
<211> 431
<212> PRT
<213> Trichoderma reesei

<400> 6
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Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20   25   30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
            35   40   45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
      50   55   60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65   70   75   80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                    85   90   95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
                    100   105   110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
            115   120   125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
      130   135   140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145   150   155   160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                    165   170   175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
                    180   185   190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
            195   200   205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
      210   215   220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225   230   235   240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                    245   250   255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
                    260   265   270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
            275   280   285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
      290   295   300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305   310   315   320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                    325   330   335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340   345   350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
      355   360   365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn

Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385   390   395   400
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                   405   410   415
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
            420   425   430

<210>   7
<211>   1077
<212>   DNA
<213>   Acidothermus cellulolyticus

<400>   7
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gtacggatcg ccggcatcaa ctggtttggg ttcgaaacct gcaattacgt cgtgcacggt   120
ctctggtcac gcgactaccg cagcatgctc gaccagataa agtcgctcgg ctacaacaca   180
atccggctgc cgtactctga cgacattctc aagcccgggc ccatgccgaa cagcatcaat   240
ttttaccaga tgaatcagga cctgcagggt ctgacgtcct tgcaggtcat ggacaaaatc   300
gtcgcgtacg ccggtcagat cggcctgcgc atcattcttg accgccaccg accggattgc   360
agcgggcagt cggcgctgtg gtacacgagc agcgtctcgg aggctacgtg gatttccgac   420
ctgcaagcgc tggcgcagcg ctacaaggga aacccgacgg tcgtcggctt tgacttgcac   480
aacgagccgc atgacccggc ctgctggggc tgcggcgatc cgagcatcga ctggcgattg   540
gccgccgagc gggccggaaa cgccgtgctc tcggtgaatc cgaacctgct catttttcgtc   600
gaaggtgtgc agagctacaa cggagactcc tactggtggg cggcaacct gcaaggagcc   660
ggccagtacc cggtcgtgct gaacgtgccg aaccgcctgg tgtactcggc cacgactac   720
gcgacgagcg tctacccgca cgtggttc agcgatccga ccttccccaa caacatgccc   780
ggcatctgga caagaactg gggatacctc ttcaatcaga acattgcacc ggtatggctg   840
ggcgaattcg gtacgacact gcaatccacg accgaccaga gtggctgaa gacgctcgtc   900
cagtacctac ggccgaccgc gcaatacggt gcggacagct ccagtggac cttctggtcc   960
tggaaccccg attccggcga cacaggagga attctcaagg atgactggca gacggtcgac   1020
acagtaaaag acggctatct cgcgccgatc aagtcgtcga ttttcgatcc tgtcggc   1077

<210>   8
<211>   359
<212>   PRT
<213>   Acidothermus cellulolyticus

<400>   8
Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg Glu Ile Leu Asp Ala
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Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn Trp Phe Gly Phe Glu
            20   25   30
Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser Arg Asp Tyr Arg Ser
         35   40   45
Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro
     50   55   60
Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn
65   70   75   80
Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val
               85   90   95
Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile
            100   105   110
Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr
         115   120   125
Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu
     130   135   140

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Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His
145                 150                 155                 160
Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile
                165                 170                 175
Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn Ala Val Leu Ser Val
                180                 185                 190
Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val Gln Ser Tyr Asn Gly
            195                 200                 205
Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly Ala Gly Gln Tyr Pro
        210                 215                 220
Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr Ser Ala His Asp Tyr
225                 230                 235                 240
Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser Asp Pro Thr Phe Pro
                245                 250                 255
Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp Gly Tyr Leu Phe Asn
                260                 265                 270
Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe Gly Thr Thr Leu Gln
            275                 280                 285
Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu Val Gln Tyr Leu Arg
        290                 295                 300
Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln Trp Thr Phe Trp Ser
305                 310                 315                 320
Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile Leu Lys Asp Asp Trp
                325                 330                 335
Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu Ala Pro Ile Lys Ser
                340                 345                 350
Ser Ile Phe Asp Pro Val Gly
        355
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<210>    9
<211>    1914
<212>    DNA
<213>    Acidothermus cellulolyticus

<400>    9
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ccggactacg ggcacgagac aacttcggag gcgtacagct tctggctctg gctcgaagcg     180
acgtacggcg cagtgaccgg caactggacg ccgttcaaca cgcctggac gacgatggaa     240
acgtacatga tcccgcagca cgcggaccag ccgaacaacg cgtcgtacaa ccccaacagc     300
ccggcgtcgt acgctccgga gagccgctg cccagcatgt acccggttgc catcgacagc     360
agcgtgccgg ttgggcacga cccgctcgcc gccgaattgc agtcgacgta cggcactccg     420
gacatttacg gcatgcactg gctggccgac gttgacaaca tctacggata cggcgacagc     480
cccggcggtg gttgcgaact cggtccttcc gctaagggcg tctcctacat caacacattc     540
cagcgcggct cgcaggagtc cgtctgggag acggtcaccc agccgacgtg cgacaacggc     600
aagtacggtg gggcgcacgg ctacgtcgac ctgttcatcc agggttcgac gccgccgcag     660
tggaagtaca ccgatgcccc ggacgccgac gcccgtgccg tccaggctgc gtactgggcc     720
tacacctg
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